

WEST Search History

Updated search

DATE: Tuesday, February 08, 2005

Hide? Set Name Query

Hit Count

DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND

<input type="checkbox"/>	L1	lee.in. or guerry.in. or burg.in.	259623
<input type="checkbox"/>	L2	L1 and (campylob\$ or campy\$)	89
<input type="checkbox"/>	L3	L2 and (plasmid or vector)	60
<input type="checkbox"/>	L4	L3 and (fla or fla-a or flaa or flagel\$ or SEQ or SEQ. or SEQ-ID).clm.	31
<input type="checkbox"/>	L5	L1 and (fla or fla-a or flaa or flagel\$ or SEQ or SEQ. or SEQ-ID).clm.	753
<input type="checkbox"/>	L6	L5 and (campyl\$ or campylobacter\$).clm.	1

END OF SEARCH HISTORY

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)Search for

NiceProt

View of

Swiss-

Prot:

P27053

Updated search 10/4/05

[Printer-friendly view](#)[Submit update](#)[Quick BlastP search](#)

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **FLAA_CAMCO**
 Primary accession number **P27053**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 23, August 1992
 Sequence was last modified in Release 34, October 1996
 Annotations were last modified in Release 44, July 2004

Name and origin of the protein

Protein name **Flagellin A**
 Synonyms None
 Gene name **Name: flaA**
 From **Campylobacter coli [TaxID: 195]**
 Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacterales; Campylobacteraceae; Campylobacter.**

References

[1] NUCLEOTIDE SEQUENCE.

STRAIN=VC167 T2;
MEDLINE=91310584;PubMed=1856171 [NCBI, ExPASy, EBI, Israel, Japan]
Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
"Role of two flagellin genes in Campylobacter motility.";
J. Bacteriol. 173:4757-4764(1991).

Comments

- **FUNCTION:** Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- **SUBUNIT:** Heteropolymer of flaA and flaB. A flagellar filament composed exclusively of flaA is indistinguishable in length from that of the wild type and shows a slight reduction in motility. The flagellar filament composed exclusively of the flaB is severely truncated in length and greatly reduced in motility. Thus, while both flagellins are not necessary for motility, both are required for a fully active flagellar filament.
- **SIMILARITY:** Belongs to the bacterial flagellin family.

Copyright

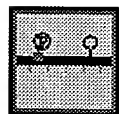
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

Cross-references

EMBL M64670; AAA23022.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 M64671; AAA23026.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 PIR A42474; A42474.
 HSSP P06179; 1UCU. [HSSP ENTRY / PDB]
 IPR001029; Flagellin_C.
 InterPro IPR010810; Flagellin_IN.
 IPR001492; Flagellin_N.
 Graphical view of domain structure.
 Pfam PF00700; Flagellin_C; 1.
 PF07196; Flagellin_IN; 2.
 PF00669; Flagellin_N; 1.
 Pfam graphical view of domain structure.
 PRINTS PR00207; FLAGELLIN.
 ProDom PD000316; Flagellin_C; 1.
 [Domain structure / List of seq. sharing at least 1 domain]
 HOBACGEN [Family / Alignment / Tree]
 BLOCKS P27053.
 ProtoNet P27053.
 ProtoMap P27053.
 PRESAGE P27053.
 DIP P27053.
 ModBase P27053.
 SMR P27053; BD97DFF6CD099004.
 SWISS-2DPAGE Get region on 2D PAGE.
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features

Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		By similarity.
VARIANT	201	202	2	DS -> QN.

Sequence information

Length: 572 Molecular weight: 58880 CRC64: BD97DFF6CD099004 [This is a checksum on the sequence]
 AA Da

10	20	30	40	50	60
GFRINTNVAA	LNAKANSDLN	SRALDQSLSR	LSSGLRINSA	ADDASGMAIA	DSLRSQANTL
70	80	90	100	110	120

```

GQAISNGNDA LGILQTADKA MDEQLKILDT IKTKATQAAQ DGQSLKTRTM LQADINRLME
      130      140      150      160      170      180
ELDNIANTTS FNGKQLLSGG FTNQEFQIGS SSNQTIKASI GATQSSKIGV TRFETGSQSF
      190      200      210      220      230      240
SSGTVGLTIK NYNGIEDFKF DSVVISTSVG TGLGALAEI NRNADKTGIR ATFDVKSQVA
      250      260      270      280      290      300
YAIKAGNTSQ DFAINGVVIG KVDYSDGDEN GSLISAINAV KDTTGVQASK DENGKLVLTG
      310      320      330      340      350      360
ADGRGIKITG SIGVGAGILH TENYGRSLV KNDGRDINIS GTGLSAIGMG ATDMISQSSV
      370      380      390      400      410      420
SLRESKGQIS AANADAMGFN AYNGGGAKQI IFASSIAGFM SQAGSGFSAG SGFSVSGSKN
      430      440      450      460      470      480
YSAILSASIQ IVSSARSISS TYVVSTGSGF SAGSGNSQFA ALRISTVSAH DETAGVTTLK
      490      500      510      520      530      540
GAMAVMDIAE TAITNLDQIR ADIGSVQNQI TSTINNITVT QVNVKSAESQ IRDVDFASES
      550      560      570
ANYSKANILA QSGSYAMAQA NSSQQNVLRL LQ

```

P27053 in FASTA
format

View entry in original Swiss-Prot format

View entry in raw text format (no links)

Report form for errors/updates in this Swiss-Prot entry

BLAST

BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Search the SWISS-MODEL Repository

ExPASy Home page		Site Map		Search ExPASy		Contact us		Swiss-Prot	
Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Brazil <small>new</small>	Canada	China	Korea	Switzerland	Taiwan


[ExPASy Home page](#)
[Site Map](#)
[Search ExPASy](#)
[Contact us](#)
[Proteomics tools](#)
[Swiss-Prot](#)

Search for

=====

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 333 AA

Date run: 2005-02-08 16:27:35 UTC+0100 on elisio.isb-sib.ch

Program: NCBI BLASTP 2.2.6 [Apr-09-2003]

Database: /work/expasy/tmp/make_blast_fasta/UniProt

1,768,175 sequences; 565,733,592 total letters

UniProt Release 4.0 consists of: Swiss-Prot Release 46.0 of 01-Feb-2005: 168297 en
TrEMBL Release 29.0 of 01-Feb-2005: 1589670 entrie

[Taxonomic view](#)

[NiceBlast view](#)

[Printable view](#)

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

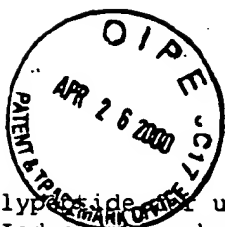
Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp P27053	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	632	e-180
<input type="checkbox"/>	tr Q9RPY6	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	624	e-178
<input type="checkbox"/>	tr Q84IB9	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...]	619	e-176
<input type="checkbox"/>	tr Q46009	_CAMCO Flagellin [Campylobacter coli]	608	e-173
<input type="checkbox"/>	sp P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...]	605	e-172
<input type="checkbox"/>	tr Q99QL6	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	593	e-168
<input type="checkbox"/>	tr Q99Q27	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	592	e-168
<input type="checkbox"/>	tr Q93NL6	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	585	e-166

<input type="checkbox"/>	tr	<u>Q93NL9</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>585</u>	e-166
<input type="checkbox"/>	sp	<u>P22251</u>	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>581</u>	e-165
<input type="checkbox"/>	tr	<u>O85179</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>581</u>	e-165
<input type="checkbox"/>	tr	<u>Q8G9F3</u>	_CAMCO Flagellin (Fragment) [flaA] [Campylobacte...	<u>581</u>	e-165
<input type="checkbox"/>	tr	<u>Q9R950</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>579</u>	e-164
<input type="checkbox"/>	tr	<u>Q9RF26</u>	_CAMJE Chimeric flagellin A/B [Campylobacter jej...	<u>577</u>	e-164
<input type="checkbox"/>	tr	<u>Q9R953</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>577</u>	e-163
<input type="checkbox"/>	tr	<u>O85183</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>575</u>	e-163
<input type="checkbox"/>	sp	<u>P22252</u>	FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>568</u>	e-161
<input type="checkbox"/>	tr	<u>Q9RF25</u>	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>568</u>	e-161
<input type="checkbox"/>	tr	<u>Q7X516</u>	_CAMJE FlaB [flaB] [Campylobacter jejuni]	<u>565</u>	e-160
<input type="checkbox"/>	sp	<u>Q46113</u>	FLA3_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>529</u>	e-149
<input type="checkbox"/>	tr	<u>Q6L5K6</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>528</u>	e-149
<input type="checkbox"/>	tr	<u>Q6L5K1</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>527</u>	e-148
<input type="checkbox"/>	tr	<u>Q6L5J8</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>526</u>	e-148
<input type="checkbox"/>	tr	<u>O30696</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>526</u>	e-148
<input type="checkbox"/>	tr	<u>Q9R952</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>525</u>	e-148
<input type="checkbox"/>	tr	<u>Q9R949</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>525</u>	e-148
<input type="checkbox"/>	tr	<u>Q84IB8</u>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...	<u>524</u>	e-148
<input type="checkbox"/>	tr	<u>Q6L5K7</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>524</u>	e-147
<input type="checkbox"/>	tr	<u>Q6L5J9</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>524</u>	e-147
<input type="checkbox"/>	tr	<u>Q6L5K8</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>523</u>	e-147
<input type="checkbox"/>	tr	<u>Q6L5K2</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>523</u>	e-147
<input type="checkbox"/>	tr	<u>O85180</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>523</u>	e-147
<input type="checkbox"/>	tr	<u>O85182</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>523</u>	e-147
<input type="checkbox"/>	tr	<u>Q8G9F2</u>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...	<u>522</u>	e-147
<input type="checkbox"/>	tr	<u>Q6L5K9</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>522</u>	e-147
<input type="checkbox"/>	sp	<u>P56963</u>	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>521</u>	e-147
<input type="checkbox"/>	tr	<u>Q6L5L0</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>521</u>	e-147
<input type="checkbox"/>	tr	<u>Q6L5J6</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>521</u>	e-147
<input type="checkbox"/>	tr	<u>O34938</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>521</u>	e-147
<input type="checkbox"/>	tr	<u>Q8G9F1</u>	_CAMCO Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr	<u>Q6L5K5</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr	<u>Q6L5K4</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr	<u>Q6L5K0</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr	<u>Q6L5J7</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>520</u>	e-146
<input type="checkbox"/>	tr	<u>O30689</u>	_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	<u>520</u>	e-146
<input type="checkbox"/>	tr	<u>Q6L5L1</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>518</u>	e-146
<input type="checkbox"/>	tr	<u>Q93NL8</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>516</u>	e-145
<input type="checkbox"/>	tr	<u>Q8G9F0</u>	_CAMJE Flagellin (Fragment) [flaA] [Campylobacte...	<u>515</u>	e-145
<input type="checkbox"/>	tr	<u>Q93NL7</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>514</u>	e-144
<input type="checkbox"/>	tr	<u>P96751</u>	_9PROT Flagellin (Fragment) [flaA] [Campylobacte...	<u>513</u>	e-144
<input type="checkbox"/>	sp	<u>Q46114</u>	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	<u>512</u>	e-144
<input type="checkbox"/>	tr	<u>Q933V4</u>	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...	<u>512</u>	e-144
<input type="checkbox"/>	tr	<u>Q6L5K3</u>	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...	<u>508</u>	e-143

<input type="checkbox"/>	tr	Q5UEG1	_CAMJE FlaA (Fragment) [flaA] [Campylobacter jej...]	508	e-143
<input type="checkbox"/>	tr	P96752	_9PROT Flagellin [flaB] [Campylobacter sp]	508	e-143
<input type="checkbox"/>	tr	O85181	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	506	e-142
<input type="checkbox"/>	sp	P56964	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	506	e-142
<input type="checkbox"/>	tr	Q79AR6	_CAMJE Flagellin [flaA] [Campylobacter jejuni]	504	e-142
<input type="checkbox"/>	tr	Q9R954	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	504	e-142
<input type="checkbox"/>	tr	Q9R951	_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	504	e-141
<input type="checkbox"/>	tr	Q5UEG2	_CAMJE FlaA (Fragment) [flaA] [Campylobacter jej...]	468	e-131
<input type="checkbox"/>	tr	Q93GT4	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	454	e-127
<input type="checkbox"/>	tr	Q93R24	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	454	e-126
<input type="checkbox"/>	tr	Q84IC3	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	445	e-124
<input type="checkbox"/>	tr	Q84IC6	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	445	e-124
<input type="checkbox"/>	tr	Q84IC7	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	442	e-123
<input type="checkbox"/>	tr	Q8RTY4	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	442	e-123
<input type="checkbox"/>	tr	Q93GT1	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	441	e-123
<input type="checkbox"/>	tr	Q84IC1	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	438	e-122
<input type="checkbox"/>	tr	Q93GT2	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	438	e-122
<input type="checkbox"/>	tr	Q84IC8	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	437	e-121
<input type="checkbox"/>	tr	Q84IC5	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	437	e-121
<input type="checkbox"/>	tr	Q84IC4	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	436	e-121
<input type="checkbox"/>	tr	Q84IC9	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	433	e-120
<input type="checkbox"/>	tr	Q93GT3	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	429	e-119
<input type="checkbox"/>	tr	Q84IC2	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	427	e-118
<input type="checkbox"/>	tr	Q84IC0	_CAMLA Flagellin (Fragment) [flaA] [Campylobacte...]	417	e-115
<input type="checkbox"/>	tr	Q46462	_CAMUP Flagellin (Fragment) [fla2] [Campylobacte...]	409	e-113
<input type="checkbox"/>	tr	Q46461	_CAMUP Flagellin (Fragment) [fla1] [Campylobacte...]	400	e-110
<input type="checkbox"/>	tr	Q56746	_WOLSU Flagellin [flag] [Wolinella succinogenes]	352	4e-96
<input type="checkbox"/>	tr	Q7X2D0	_HELPHY Flagellin B [flaB] [Helicobacter pylori (...]	350	2e-95
<input type="checkbox"/>	tr	Q7M7N1	_WOLSU FLAGELLIN B [FLAB] [Wolinella succinogenes]	347	1e-94
<input type="checkbox"/>	sp	Q07911	FLAB_HELPHY Flagellin B (Flagellin N) [flaB] [Helicobac...]	347	2e-94
<input type="checkbox"/>	sp	Q92MV8	FLAB_HELPHY Flagellin B (Flagellin N) [flaB] [Helicobac...]	347	2e-94
<input type="checkbox"/>	tr	Q8RNU8	_HELPHY Flagellin B subunit [flaB] [Helicobacter ...]	347	2e-94
<input type="checkbox"/>	tr	Q6VYQ1	_HELPHY Flagellin B (FlaB) [flaB] [Helicobacter p...]	347	2e-94
<input type="checkbox"/>	tr	Q8GD49	_HELPHY Flagellin [flaB] [Helicobacter pylori (Ca...]	346	4e-94
<input type="checkbox"/>	tr	Q7X2D1	_HELPHY Flagellin A [flaA] [Helicobacter pylori (...]	344	2e-93
<input type="checkbox"/>	sp	Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	342	5e-93
<input type="checkbox"/>	sp	Q03843	FLAA_HELPHY Flagellin A [flaA] [Helicobacter pylori (Ca...]	340	3e-92
<input type="checkbox"/>	tr	Q64EY2	_HELPHY FlaA [flaA] [Helicobacter pylori (Campylo...]	340	3e-92
<input type="checkbox"/>	tr	Q9XB37	_HELFE Flagellin B [flaB] [Helicobacter felis]	338	9e-92
<input type="checkbox"/>	tr	Q7TTM9	_HELHP Major flagellin subunit FlaA_1 (Major fla...]	338	1e-91
<input type="checkbox"/>	sp	Q07910	FLAB_HELPHU Flagellin B (Flagellin N) [flaB] [Helicobac...]	337	2e-91
<input type="checkbox"/>	tr	Q6VYQ2	_HELPHY Flagellin A [flaA] [Helicobacter pylori (...]	336	3e-91
<input type="checkbox"/>	tr	Q93NM0	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	332	6e-90
<input type="checkbox"/>	tr	Q93NM1	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	332	8e-90
<input type="checkbox"/>	tr	Q933J6	_CAMJE Flagellin A (Fragment) [flaA] [Campylobac...]	330	2e-89

SEQUENCE LISTING

<110> Guerry, Patricia
Trust, Trevor J
Burg, Edward
Lee, Lanfong



<120> A Recombinant Polypeptide for use in the Manufacture of Vaccines
against Campylobacter Induced Diarrhea and to Reduce Colonization

<130> 78560

<140>

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 999

<212> DNA

<213> Campylobacter coli

<400> 1

```

attaacacaa atgttgacgc attaaatgct aaagcaaatt cggatctaaa cagcagagca 60
ttagatcaat cactttcaag actcagttca ggtcttagaa tcaactccgc agcagatgat 120
gcttcaggga tggcgatagc agatagttaa agatctcagg caaatacttt gggtcaggct 180
atatctaata gtaatgatgc tttaggtatc ttgcaaaactg cagataaggc tatggatgag 240
caacttaaaa tcttagatac catcaagact aaagcgactc aagctgctca agatgggtcaa 300
agcttaaaaa caagaactat gcttcaagca gacatcaacc gtttgatgga agaacttgat 360
aatatcgcaa ataccacttc atttaatggc aaacaacttt taagtgggtg ttttaccaat 420
caagaattcc aaatcggttc aagttcaaat caaactatta aagcaagtat aggagcaact 480
cagtcttcta aaatcggtgt aacaagattt gaaacagggt caciaaagttt ttcttcaggc 540
actgtaggac ttactattaa aaactacaac ggtatcgaag attttaaat tgatagtgt 600
gtgatttcta cttcagtagg aacaggtctt ggagctttgg ctgaagagat caacagaaat 660
gcagataaaa caggaattcg tgcaactttt gatgtaaaat ctgtaggagc ctatgcaata 720
aaagcaggaa atacttctca ggattttgct atcaatgggg ttgttatagg taaggttgat 780
tattcagatg gtgatgagaa tgggtcttta atttcagcta tcaatgctgt aaaagataca 840
actggtgttc aagcctctaa agatgaaaat ggtaaacttg ttcttacttc ggccgatggt 900
agagggatta aaatcacagg tagcataggt gtaggagctg gtatattgca cactgaaaat 960
tatggaaggt tatctttagt taaaaatgat ggtagagat 999

```

<210> 2

<211> 333

<212> PRT

<213> Campylobacter coli

<400> 2

```

Ile Asn Thr Asn Val Ala Ala Leu Asn Ala Lys Ala Asn Ser Asp Leu
1           5           10           15
Asn Ser Arg Ala Leu Asp Gln Ser Leu Ser Arg Leu Ser Ser Gly Leu
20           25           30
Arg Ile Asn Ser Ala Ala Asp Asp Ala Ser Gly Met Ala Ile Ala Asp
35           40           45
Ser Leu Arg Ser Gln Ala Asn Thr Leu Gly Gln Ala Ile Ser Asn Gly
50           55           60
Asn Asp Ala Leu Gly Ile Leu Gln Thr Ala Asp Lys Ala Met Asp Glu
65           70           75           80

```

Personnel <141>

Gln	Leu	Lys	Ile	Leu	Asp	Thr	Ile	Lys	Thr	Lys	Ala	Thr	Gln	Ala	Ala
85					90					95					
Gln	Asp	Gly	Gln	Ser	Leu	Lys	Thr	Arg	Thr	Met	Leu	Gln	Ala	Asp	Ile
100					105					110					
Asn	Arg	Leu	Met	Glu	Glu	Leu	Asp	Asn	Ile	Ala	Asn	Thr	Thr	Ser	Phe
115					120					125					
Asn	Gly	Lys	Gln	Leu	Leu	Ser	Gly	Gly	Phe	Thr	Asn	Gln	Glu	Phe	Gln
130					135					140					
Ile	Gly	Ser	Ser	Ser	Asn	Gln	Thr	Ile	Lys	Ala	Ser	Ile	Gly	Ala	Thr
145					150					155					160
Gln	Ser	Ser	Lys	Ile	Gly	Val	Thr	Arg	Phe	Glu	Thr	Gly	Ser	Gln	Ser
165					170					175					
Phe	Ser	Ser	Gly	Thr	Val	Gly	Leu	Thr	Ile	Lys	Asn	Tyr	Asn	Gly	Ile
180					185					190					
Glu	Asp	Phe	Lys	Phe	Asp	Ser	Val	Val	Ile	Ser	Thr	Ser	Val	Gly	Thr
195					200					205					
Gly	Leu	Gly	Ala	Leu	Ala	Glu	Glu	Ile	Asn	Arg	Asn	Ala	Asp	Lys	Thr
210					215					220					
Gly	Ile	Arg	Ala	Thr	Phe	Asp	Val	Lys	Ser	Val	Gly	Ala	Tyr	Ala	Ile
225					230					235					240
Lys	Ala	Gly	Asn	Thr	Ser	Gln	Asp	Phe	Ala	Ile	Asn	Gly	Val	Val	Ile
245					250					255					
Gly	Lys	Val	Asp	Tyr	Ser	Asp	Gly	Asp	Glu	Asn	Gly	Ser	Leu	Ile	Ser
260					265					270					
Ala	Ile	Asn	Ala	Val	Lys	Asp	Thr	Thr	Gly	Val	Gln	Ala	Ser	Lys	Asp
275					280					285					
Glu	Asn	Gly	Lys	Leu	Val	Leu	Thr	Ser	Ala	Asp	Gly	Arg	Gly	Ile	Lys
290					295					300					
Ile	Thr	Gly	Ser	Ile	Gly	Val	Gly	Ala	Gly	Ile	Leu	His	Thr	Glu	Asn
305					310					315					320
Tyr	Gly	Arg	Leu	Ser	Leu	Val	Lys	Asn	Asp	Gly	Arg	Asp			
325					330										

<210> 3

<211> 27

<212> DNA

<213> Campylobacter coli

<400> 3

accaatatta acacaaatgt tgcagca

27

<210> 4

<211> 33


<212> DNA

<213> Campylobacter coli

<400> 4

ttatctagac taatctctac catcattttt aac

33

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
--	--------------------------	-------------------------------	----------------------------	----------------------------

Search for

NiceProt

View of

TrEMBL:

O30688

[Printer-friendly view](#)
[Request update](#)
[Quick BlastP search](#)

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **O30688_CAMCO**
 Primary accession number **O30688**
 Secondary accession numbers None
 Entered in TrEMBL in Release 05, January 1998
 Sequence was last modified in Release 05, January 1998
 Annotations were last modified in Release 24, June 2003

Name and origin of the protein

Protein name **Flagellin A [Fragment]**
 Synonyms None
 Gene name **Name: flaA**
 From **Campylobacter coli [TaxID: 195]**
 Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacterales; Campylobacteraceae; Campylobacter.**

References

- [1] NUCLEOTIDE SEQUENCE.
STRAIN=D1159;
 Meinersmann R.J., Helsel L.O., Fields P.I., Hiatt K.L.;
 "Discrimination of *Campylobacter jejuni* by fla gene sequencing."; *J. Clin. Microbiol.* 0:0-0(1997).

Comments

None

Cross-references

EMBL **AF015091; AAB69353.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]**
GO:0009420; Cellular component: flagellar filament (sensu Bacteria) (inferred from electronic annotation).
GO:0019861; Cellular component: flagellum (inferred from electronic annotation).
 GO **GO:0005198; Molecular function: structural molecule activity (inferred from electronic annotation).**
GO:0001539; Biological process: ciliary or flagellar motility (inferred from electronic annotation).

QuickGo
view.

InterPro IPR001492; Flagellin_N.
Graphical view of domain structure.

Pfam PF00669; Flagellin_N; 1.
Pfam graphical view of domain structure.

ProtoMap O30688.

PRESAGE O30688.

ModBase O30688.

SMR O30688; A1EBB1B61699B04D.

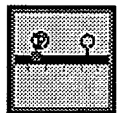
SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features



Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	89	89		

Sequence information

Length: **89 AA** [This is the length of the partial sequence] Molecular weight: **9630 Da** [This is the MW of the partial sequence] CRC64: **A1EBB1B61699B04D** [This is a checksum on the sequence]

10	20	30	40	50	60
QDGQSLKTRT	MLQADINRLM	EELDNIAINTT	SFNGKQLLSG	NFINQEFQIG	ASSNQTVKAT
70	80				
IGATQSSKIG	LTRFETGGRI	SSSGEVQFT			

O30688 in FASTA
format

View entry in original TrEMBL format

View entry in raw text format (no links)

Request for annotation of this TrEMBL entry

BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)




Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Search the SWISS-MODEL Repository

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
--	--------------------------	-------------------------------	----------------------------	----------------------------

Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Brazil new	Canada	China	Korea	Switzerland	Taiwan
----------------------	------------------	-----------	---------	-------------------	--------	-------	-------	-------------	--------



Get for ? Site search



EBI Home About EBI Research Services Toolbox **Databases** Downloads

DATABASE BROWSING

EBI Dbfetch

```

ID      CCFLAA      standard; genomic DNA; PRO; 4200 BP.
XX
AC      M64670;
XX
SV      M64670.1
XX
DT      01-MAY-1991 (Rel. 28, Created)
DT      05-JUL-1999 (Rel. 60, Last updated, Version 3)
XX
DE      C.coli flagellin (flaA and flaB) genes, complete cds.
XX
KW      flagellin.
XX
OS      Campylobacter coli
OC      Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC      Campylobacteraceae; Campylobacter.
XX
RN      [1]
RP      1-4200
RX      MEDLINE; 91310584.
RX      PUBMED; 1856171.
RA      Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
RT      "Role of two flagellin genes in Campylobacter motility";
RL      J. Bacteriol. 173(15):4757-4764(1991).
XX
FH      Key          Location/Qualifiers
FH
FT      source          1..4200
FT                        /db_xref="taxon:195"
FT                        /mol_type="genomic DNA"
FT                        /organism="Campylobacter coli"
FT                        /strain="VC167-T1"
FT      gene          240..2108
FT                        /gene="flaA"
FT      -35 signal      240..244
FT                        /note="the -35 region for the flaA gene of VC167-T2;
FT                        putative"
FT                        /gene="flaA"
FT      -10 signal      262..267
FT                        /note="'The Pribnow box for the flaA flagellin gene from C.
FT                        coli VC167-T2'; putative"
FT                        /gene="flaA"
FT      RBS          309..312
FT                        /note="'RBS for flaA'; putative"
FT                        /gene="flaA"
FT      CDS          319..2040
FT                        /codon_start=1
FT                        /db_xref="GOA:P27053"
FT                        /db_xref="HSSP:O67803"
FT                        /db_xref="UniProt/Swiss-Prot:P27053"
FT                        /note="'the open reading frame encoding flaA'; putative"
FT                        /transl_table=11
FT                        /product="flagellin"

```

```

FT      /gene="flaA"
FT      /protein_id="AAA23022.1"
FT      /translation="MGFRINTNVAALNAKANSDLNSRALDQSLRLSSGLRINSAADDA
FT      SGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGO
FT      SLKTRTMLQADINRLMEELDNIAINTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGA
FT      TQSSKIGVTRFETGSQSFS SGTVGLTIKNYNGIEDFKFDSVVIISTSVGTGLGALAEIN
FT      RNADKTGIRATFDVKS VGAYAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAV
FT      KD TTGVQASKDENGKLVLT SADGRGIKITGSIGVGAGILHTENYGRSLVKNDGRDINI
FT      SGTGLSAIGMGATDMISQSSVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSIAG
FT      FMSQAGSGFSAGSGFSVGSGKNYSAILSASIQIVSSARSISSTYVVSTGSGFSAGSGNS
FT      QFAALRISTVSAHDETAGVTT LKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINN
FT      ITVTQVNVKSAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQONVLRLLQ"
FT      terminator      2085..2108
FT      /note="'the putative transcriptional terminator following
FT      flaA'; putative"
FT      /gene="flaA"
FT      misc signal      2149..2150
FT      /label=-26_signal-flaB
FT      /note="putative"
FT      /gene="flaB"
FT      gene      2149..3922
FT      /gene="flaB"
FT      misc signal      2161..2162
FT      /label=-13_signal-flaB
FT      /note="putative"
FT      /gene="flaB"
FT      RBS      2191..2194
FT      /note="'RBS for flaB'; putative"
FT      /gene="flaB"
FT      CDS      2201..3922
FT      /codon_start=1
FT      /db_xref="GOA:P18245"
FT      /db_xref="HSSP:O67803"
FT      /db_xref="UniProt/Swiss-Prot:P18245"
FT      /note="'the open reading frame encoding flaB'; putative"
FT      /transl_table=11
FT      /product="flagellin"
FT      /gene="flaB"
FT      /protein_id="AAA23023.1"
FT      /translation="MGFRINTNIGALNAHANSVVNARELDKSLRLSSGLRINSAADDA
FT      SGMAIADSLRSQAATLGQAINNNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGO
FT      SLKTRTMLQADINRLMEELDNIAINTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGA
FT      TQSSKIGVTRFETGSQSFS SGTVGLTIKNYNGIEDFKFDSVVIISTSVGTGLGALAEIN
FT      RNADKTGIRATFDVKS VGAYAIKAGNTSQDFAINGVVIGQINYNDDGNNQQLISAINAV
FT      KD TTGVQASKDENGKLVLT SADGRGIKITGSIGVGAGILHTENYGRSLVKNDGRDINI
FT      SGTGLSAIGMGATDMISQSSVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSIAG
FT      FMSQAGSGFSAGSGFSVGSGKNYSAILSASIQIVSSARSISSTYVVSTGSGFSAGSGNS
FT      QFAALRISTVSAHDETAGVTT LKGAMAVMDIAETAITNLDQIRADIGAVQNQLQVTINN
FT      ITVTQVNVKAAESTIRDVDFAAESANFSKYNILAQSGSYAMSQRNAVQQNVKLKLQ"

```

```

XX      Sequence 4200 BP; 1393 A; 659 C; 834 G; 1314 T; 0 other;
SQ      ttttagtgat gataacttta tacagtggt attttaaag gggatttgta ttatcgtagg      60
      agttttttat ctgaagctat aaaaaaagat ttgaaagatg aggcgtatta tcttttaaat      120
      tttattagcg cttatcaaaa atggcttgaa aagtttattg agaggctaga aataaaaaat      180
      gccatcataa aagatacagt gttaaaatat ggaaatttga tataaaattt tataaaactc      240
      taaactatth ttctttttaa acgatatagt ttataacaag ttcatggatg gacttgaatt      300
      tattttaaag gattttaaag gggatttcgt attaacacaa atgttgcagc attaaatgct      360
      aaagcaaat cggatctaaa cagcagagca ttagatcaat cactttcaag actcagttca      420
      ggtcttagaa tcaactccgc agcagatgat gcttcagga tggcgatagc agatagttha      480
      agatctcagg caaatacttt gggtcaggct atatctaag gtaatgatgc tttaggatgc      540
      ttgcaaacg cagataaggc tatggatgag caacttaaaa tcttagatac catcaagact      600
      aaagcgactc aagctgctca agatggtcaa agcttaaaaa caagaactat gcttcaagca      660
      gacatcaacc gtttgatgga agaacttgat aatatcgcaa ataccacttc atttaatggc      720
      aaacaacttt taagtgggtg ttttaccact caagaattcc aaatcggttc aagttcaaat      780
      caaactatta aagcaagtat aggagcaact cagtcctcta aaatcggtgt aacaagattt      840
      gaaacaggtt cacaaagttt ttcttcaggc actgtaggac ttactattaa aaactacaac      900
      ggtatcgaag attttaaatt tgatagtgta gtgatttcta cttcagtagg aacaggtctt      960

```

ggagcttttg	ctgaagagat	caacagaaat	gcagataaaa	caggaattcg	tgcaactttt	1020
gatgtaaaat	ctgtaggagc	ctatgcaata	aaagcaggaa	atacttctca	ggattttgct	1080
atcaatgggg	ttgttatagg	taagggtgat	tattcagatg	gtgatgagaa	tggttcttta	1140
atttcagcta	tcaatgctgt	aaaagataca	actggtgttc	aagcctctaa	agatgaaaat	1200
ggtaaacctt	ttcttacttc	ggcggatggt	agagggatta	aaatcacagg	tagcatagggt	1260
gtaggagctg	gtatattgca	cactgaaaat	tatggaaggt	tatctttagt	taaaaatgat	1320
ggtagagata	tcaatataag	tggaacaggt	ctttcagcta	taggtatggg	tgctacagac	1380
atgattttct	aatcttcagt	atctctaaga	gagtcaaaag	ggcaaatttc	agcagccaat	1440
gctgatgcta	tgggctttta	tgcttataat	ggcggcggcg	ctaagcaaat	tattttcgct	1500
tctagtattg	caggatttat	gtctcaggct	ggttcaggct	tctctgctgg	ttcgggattt	1560
tcagttagta	gtggtaaaa	ttattcagcc	attttatcag	cttctataca	gatagtatct	1620
agcgcacgtt	ctatcagtag	cacctatggt	gtttctactg	gttcagggtt	ctctgctggg	1680
tcaggtaatt	ctcaatttgc	agctttaaga	ataagtacag	taagtgtctc	tgatgaaact	1740
gcagggtgta	ctacacttaa	gggtgcaatg	gctgtgatgg	atatagcaga	aactgctatt	1800
accaatcttg	atcaaatac	agcggatata	ggttctgtgc	aaaatacaat	cacatcgact	1860
ataaacaaca	ttactgtaac	ccaggtaaat	gttaaatcag	cagaatcaca	aatcagagat	1920
gtagattttg	caagcgagag	tgcaaattac	tctaaagcaa	atatattggc	tcaaagtggg	1980
tcttaatgta	tggtctaaag	aaattcaagc	cagcaaaatg	ttttaagatt	actacagtag	2040
tatataaaac	attctttagc	gtttactgta	atttatcaaa	atccaagcct	agtagtaata	2100
ctaggcctttt	tttattttcta	aataaaaatt	caatttgaat	caaaacttgg	aacacttctt	2160
gctttaatct	tttcgatgca	atattttgaa	aggattttaa	atgggtttta	gaataaacac	2220
caacatcggg	gcattgaacg	cacatgcaaa	ttcagttggt	aatgctaggg	agcttgacaa	2280
gtctttaagt	agacttagct	caggctcttag	aatcaactcc	gcagcagatg	atgcttcagg	2340
gatggcgata	gcagattctt	tgcggtcaca	agcagcaact	ttaggtcaag	ctataaacaa	2400
tggttaatgat	gctatagcta	tcttgcaaac	tgcagataag	gctatggatg	agcaacttaa	2460
aatcttagat	accatcaaga	ctaaagcgac	tcaagctgct	caagatgggtc	aaagcttaaa	2520
aacaagaact	atgcttcaag	cagacatcaa	ccgtttgatg	gaagaacttg	ataatatcgc	2580
aaataccact	tcattttaatg	gcaaacact	tttaagtggg	ggttttacca	atcaagaatt	2640
ccaaatcggg	tcaagttcaa	atcaaaactat	taaagcaagt	ataggagcaa	ctcagtcctc	2700
taaaatcggg	gtaacaagat	ttgaaacagg	ttcacaaagt	ttttcttcag	gcactgtagg	2760
acttactatt	aaaaactaca	acggtatcga	agatttttaa	tttgatagtg	tagtgatttc	2820
tacttcagta	ggaacaggct	ttggagcttt	ggctgaagag	atcaacagaa	atgcagataa	2880
aacaggaatt	cgtgcaactt	ttgatgtaaa	atctgtagga	gcctatgcaa	taaaagcagg	2940
aaatacttct	caggattttg	ctatcaatgg	ggttgttatc	ggacaaataa	attataatga	3000
cggtgataac	aatgggtcaac	ttatctcagc	tatcaatgct	gtaaaagata	caactgggtg	3060
tcaagcctct	aaagatgaaa	atggtaaaact	tggtcttact	tcggccgatg	gtagagggat	3120
taaaatcaca	ggtagcatag	gtgtaggagc	tggtatatgt	cacactgaaa	attatggaag	3180
gttatcttta	gttaaaaatg	atggtagaga	tatcaatata	agtggaacag	gtctttcagc	3240
tataggtatg	gggtctacag	acatgatttc	tcaatcttca	gtatctctaa	gagagtcaaa	3300
agggcaaatt	tcagcagcca	atgctgatgc	tatgggcttt	aatgcttata	atggcggcgg	3360
cgctaagcaa	attattttcg	cttctagtat	tgaggatttt	atgtctcagg	ctgggttcagg	3420
cttctctgct	ggttcgggat	tttcagtagg	tagtggtaaa	aattattcag	ccattttatc	3480
agcttctata	cagatagtat	ctagcgcacg	ttctatcagt	agcacctatg	ttgtttctac	3540
tggttcagggt	ttctctgctg	gttcaggtaa	ttctcaattt	gcagctttta	gaataagtac	3600
agtaagtgtc	atcatgaaa	ctgcagggtg	aactacactt	aagggtgcaa	tggtgtgat	3660
ggatatagca	gaaactgcta	ttaccaatct	tgatcaaatc	agagcagata	taggtgctgt	3720
gcaaaatcag	ctccaagtaa	cgataaataa	tattaccgta	acccaggtaa	atgttaaagc	3780
agcagaatca	accataagag	atgtggattt	cgctgcagaa	agtgc aaatt	tttctaagta	3840
caatatcctt	gcgcagtcgg	gttcatatgc	tatgagccaa	cgtaacgctg	tgcaacaaaa	3900
tgtcttaaaa	cttttacaat	aatttttcta	aagagcaaat	ttttgctctt	tagattaaat	3960
ttcttttttc	taattcatct	tgtaaaggga	taatggcttt	tttaattctt	atgttttgac	4020
tttctatgag	atcaattata	gtttcaatta	aagattcggt	agcataaatc	caagatagaa	4080
ttttattttg	tctttggctt	tcattgttaa	cactttggat	ataaataggg	gcaattaaac	4140
tttcttcatg	atatagacta	ggtcctaaaa	tttcatgtaa	aaaaaagtat	cttttcttgc	4200

//

[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)Search for

NiceProt

View of

TrEMBL:

Q9WW79

[Printer-friendly view](#)[Request update](#)[Quick BlastP search](#)

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#)
[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name **Q9WW79_CAMCO**
 Primary accession number **Q9WW79**
 Secondary accession numbers **None**
 Entered in TrEMBL in **Release 12, November 1999**
 Sequence was last modified in **Release 12, November 1999**
 Annotations were last modified in **Release 19, December 2001**

Name and origin of the protein

Protein name **Flagellin A [Fragment]**
 Synonyms **None**
 Gene name **Name: flaA**
 From **Campylobacter coli [TaxID: 195]**
 Taxonomy **Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacterales; Campylobacteraceae; Campylobacter.**

References

[1] NUCLEOTIDE SEQUENCE.

Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S., Candrian U.;
 "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter coli PCR products
 amplified directly from environmental samples.";
 Food Sci. Technol. 31:337-345(1998).

[2] NUCLEOTIDE SEQUENCE.

Studer E.;
 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

GO **GO:0019861; Cellular component: flagellum (inferred from electronic annotation).**
QuickGo view.
 ProtoMap **Q9WW79.**
 PRESAGE **Q9WW79.**
 ModBase **Q9WW79.**

SMR Q9WW79; C7C0EFB7A1739156.

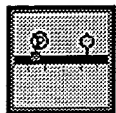
SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features



Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		

Sequence information

Length: 14 AA [This is the length of the partial sequence]

Molecular weight: 1611 Da [This is the MW of the partial sequence]

CRC64: C7C0EFB7A1739156 [This is a checksum on the sequence]

¹⁰
QANSVQQNVL RLLQ

Q9WW79 in FASTA format

View entry in original TrEMBL format

View entry in raw text format (no links)

Request for annotation of this TrEMBL entry

BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Search the SWISS-MODEL Repository

ExPASy Home page		Site Map		Search ExPASy		Contact us		Swiss-Prot	
Hosted by NCSC US	Mirror sites:	Australia	Bolivia	Brazil <small>new</small>	Canada	China	Korea	Switzerland	Taiwan